

CATGAAGGTTCCCTGTCTGCTTCTGTCCTCAGTGCAGACTTGAGCAACCGCAGGTGTCAGTCAG  
 AGCATCCCAGCATGGAGGCAGCCCTGACCGGCCCCAACGCCCTCCTCGCACTTCTGGGCCAACTACACTTCTCTGAC  
 TGGCAGAACTTGTGGCAGGAGACGTATGGGCCGAGTCCCAGAACCCACGGTGAAAGCACTGCTCATCGTGGC  
 CTACTCATTACCACATCGCTTCTCGCTTCCGTAATGTCTGGTCTGTCATGTCATCTCAAGAACCGCAGCATGC  
 ACTCGGCCACCAGCCTCTCATGTCAACCTGGCAGTGGGGACATCATGATCACATTGCTCAACACGCCCTTCACT  
 TTGGTGTGCTTGTGAACAGCACATGGGTGTTGGAAAGGGCATGTGTATGTCAGTCAGTCGCTTGCTAGTACTGTTC  
 TCTACATGTCAGCACTGACTCTGACAGCTATCGCAGTGGACCGCCACCAGGTATGTCATCCACTGAAGCCTC  
 GGATCCTCATCACCAAGGGTGTATATATATTGCTGTATCTGGGTATGGCTACCTTCTCTCTGCCACATGCC  
 ATCTGOCAGAAACTGTTACCTCAAGTACAGTGAGGACATTGTGCGCTCCCTCTGCCCTGCCGACTTCCGGAGCC  
 AGCTGACCTCTCTGGAAGTATCTGGACCTGGCCACCTCATCCTGCTTACCTACTTCCACTCTTCATTATCTCAG  
 TGGCCTATGTCGTGTGGCCAAGAAGCTGTGGCTCTGTAACACCATTGGCAGCGTGACCACAGAGCAGTACCTCGCC  
 CTGCGACGCCAGAAGAAGAACCCGCTGAAGATGCTGGCTGTGGTAGTCCCTCTTTGCCCTCTGCTGGTTCCCTCT  
 GAACTGCTATGTCCTCTCTGTCAGCAAGGCCATCCACACCAAAATGCCCTCTACTTTGCCCTCCACTGGTTTG  
 UCATGAGCAGTACTTGTATAACCCCTCATCTACTGCTGGCTCAATGAGAACCTTGGGTTGAGCTTAAGGCATTG  
 CTGAGCATGTGCCAAAGGCCACCCAAGCCGAGGAAGACAGGCTACCCCTCCCCAGTTCCCTCCAGATCCAGTCTGGGAAGA  
 CAGAGAGAGGCCATGGCGAGGGCTCCACTACCTAATCACCACTTGCCCTCTTCCAGATCCAGTCTGGGAAGA  
 CAGATCTGTCATCTGAGGAACCCGTTGTGGCATGAGTTAGGGAAAGCTGGAGATTGGTGGGGAGGGTTCTTCCT  
 CCTACAATTGACCAGACACTAACAGAGTTGAAAGTAACACAGAACAGCAGTGAGATGCTTGGGTTCTAGGAACCTGT  
 CCAGCCCCATCTGATTGCAAACCTTCTAGAAGATGCCATGAGGTGGCTGTGTAGATCTTGAGCAAGAGCTCTGG  
 AAACCCACTCAGCTTCAACAGAGGCTGGTCAGTCAACCACCTCAATTGTGTAGCATCTGCCACCTTGCCCTTCCT  
 ACTGCTGAGCAACCACAGGGGACTTGAGCCTACTAATGGTGGGCTGCCACATGCTCAGAAAAGAACAGGCAC  
 AAAGCTTCTGAAGTCAATTGAAACAGGAATAATCACACAGCTCAGTGACCTTGGCTTATCCATGACCAGACAGG  
 ACCAATTGGCTTCTAAAAACAAAGAGAAATTAGTATTGCCACTTTGAAAGTTCAAGAAAGTAAAGAAATGAGT  
 TCAGCCCTCAATTGAAAAAGAAAAAGAAAAAGAAAAAGAAAGAAAAAGCCTGTTAATATGCTGTA  
 AATTAACTGTAGCTTGCCTCTGTGTGTACATTGTACTTTAAATCTGAACACTACAGTGTCCATGTAGAT  
 TGTAATTAGCAAGAAACTGGAATATATCAGAGTATTATGAAATT (SEQ ID NO:1)

MKVPPVLLLFLLSSVRATEQPQVVTEHPSMEAALTGPNASSFWANYTFSDWQNFGRRRYGAESQNPTVKALLIVA  
 YSFTIVFSLFGNVLVCHVIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTLVRVNSTW/FGKGMCHVSRAQYCS  
 LHVSALTLTIAIVDRHQVIMHPLKPRISITKGVIYIAVIW/MATFFSLPHAIQKLFTFKYSEDIVRSLCLPDFPEP  
 ADLFWKYLDLATFILLYLLPLFIISVAYARVAKLWLNTIGDVTTEQYLALRRKKKTTVKMLVLVVVLFALCWFPPL  
 NCYVLLLSSKAIHTNNALYFAFHWFAMSSTCYNPFIYCWLNENFRVELKALLSMCQRPPKPQEDRLPSPVPSFRVAW  
 TEKSHGRRAPLPNHLPSSQIQSGKTDSSVEPVVAMS (SEQ ID NO:2)

## FIGURE 1

Underlined = deleted in targeting construct

**Bold** = sequence flanking Neo insert in targeting construct

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GGGGTGGCAGTCGGCACCATCAGGCTCCCTGGCGTTGGAGTTTCTCTGTGGTCCC
ACTCTCCGGAGGATCTCGGTTGTCTCCAAAGTCGGAACCTGGCACGGTCCAGGTTCACTC
GGAGGTCCGGGTTCCCTGTGCCCCGTGCCCTCGCTCCAGGCTCCCTGTGGTGTG
GACTCCTCTAGCCGGTGCCTCAGCCCTCGCACCCAGCCTCAGGCACAGAGCCGGC
AGGGAGCTCAGCCCTGTGCCTAGAGCTGCAGTGGCTGGACATGAAGGTTCCCTGTCC
TGCTTCTCTTCTTGTCCTAGTCGAGCTACTGAGCAACCGCAGGTCGTCACTGAGC
ATCCCAGCATGGAGGCAGGCCCTGACCGGGCCCAACGCCCTCGCACTTCTGGGECAACT
ACACTTCTCTGACTGGCAGAACATTCTGGGCAGGAGACGTTATGGGGCCGAGTCCCAGA
ACCCCAACGGTGAAGGCACTGCTCATGTCGCTACTCATTCACCATGCTCTCGCTCT
TCGGTAATGTCTGGTCTGTCTGTCATCTCAAGAACCGCAGCATGCACTCGGCCACCA
GCCTCTTCATTGTCAACCTGGCAGTGGCGACATCATGATCACATTGCTCAACACGCCCT
TCACTTTGGTCCGCTTGTGAACAGCACATGGGTGTTGGAAAGGGCATGTGTATGTCA
GTGCGTTGCTCAGTACTGTTCTACATGTCTCAGCACTGACTCTGACAGCTATCGCAG
TGGACCGCCACCAGGTCATCATGCATCCACTGAAGCCTGGATCTCCATCACCAAGGGTG
TCATATATATTGCTGTCATCTGGTCTGCTACCTCTTCTCTGCCACATGCCATCT
GCCAGAAACTGTTACCTCAAGTACAGTGAGGACATTGTGCGCTCCCTCTGCCCTGCCGG
ACTTCCCGGAGCCAGCTGACCTCTTCTGGAAAGTATCTGGACCTGGCCACCTTCATCTGC
TCTACCTACTTCCACTCTTCATTATCTCAGTGGCTATGCTGTTGGCCAAGAAGCTGT
GGCTCTGTAACACCAATTGGCAGCTGACCACAGAGCAGTACCTCGCCCTGCCACGCAAGA
AGAAGACCAACCGTGAAGATGCTGGTCTTGTGAGTCCTTGCCTGCTGGTCC
CTCTCAACTGCTATGCTCCCTCTGTCCAGCAAGGCCATCCACACCAAAATGCCCTCT
ACTTTGCCCTTCCACTGGTTGCACTGAGCACTGTTATAACCCCTTCATCTACTGCT
GGCTCAATGAGAACCTTGGGTTGAGCTTAAGGCATGAGCATGTCACAAAGGCCAC
CCAAGCCGAGGACAGGCTACCCCTCCAGTTCTCTCCAGGGTGGCATGGACAG
AGAAGAGCCATGGTCGGAGGGCTCCACTACCTAATCACCACTTGCCCTCTCCAGATCC
AGTCTGGAAAGACAGATCTGTCATCTGTGGAACCCGTGTTGGCATGAGTTAGGAAAGC
TGGAAGTTGGTGGGGAGGGTTCTTCCTCACAATTGACCAAGACACTAACAGAGTTGG
AAAGTAACACAGAACAGCAGTGAGATGCTGGGTTCTAGGAACCTGTCCAGCCCCATCTGA
TTTGCAAACACTTCTAGAAGATGCCATGAGGTGGTGTGAGATCTTGTGAGCAAGAGCTC
TGGAAACCAACCTCACTTCAACAGAGGCTGGTCCAGTCACCAACCTOCAATTGTGAGCA
TCTGCCACCTGCCCTCTACTGCTGAGCAACCACAGGGGACTTGAGCATACTATTG
GTGGGCTGCCACATGCTCAGAAAAGAACAGGCACAAAGGCTTCTGAAGTCATTGGA
ACAGGAATAATCACACAGCTCAGTGACCTTGGCTCTATCCATGACCAGACAGGACCCAT
TTTGGCTTCTAAAAACAAAGAGAAATTAGTATTGCCACTTGTGAAAGTTCAAGAAAAGTA
AAGAAATGAGTTCAAGCCCTCAATTGTAAAAAAAAGGAAAAAGAAAAAAAAGAAAAAAG
AAAGAAAAAAGCCTGTTAAATGCTGTAAATTATCTGTAGCTTGCCTTGTGTGTGT
ACATTGTACTTTAAAATCCTGAACACTACACGTGTCATGTAGATTGTAATAATTAGCAA
GAAACTGGAATATATCAGAGTATTATTGAATTC

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FIGURE 2A

Gene Sequence Structure \*      299 bp      Sequence Deleted      753 bp

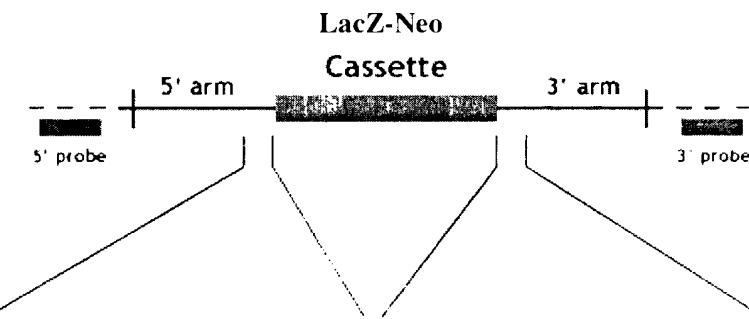
Size of partial  
cDNA: 2253 bp



Targeting Vector\*  
(genomic sequence)

Construct Number: 463

Arm Length:  
5': 2.5 kb  
3': 0.6 kb



— Targeting Vector  
- - - Endogenous Locus

\* Not drawn to scale

<pre>5' &gt;CTGGCACGSTCCAGGTTCACT CGGAGGOCGCCGGCTTCCTCTGTGC CCCGTGCCTCTCGTCCCTGGCTC CCTCTGTGGTGTGGACTCCTCTAG CCCGGTGCGCTCAGGCCCTCGCAC CCAGGCTCCAGGCACAGAGGCCGG CAGGGAGCTCAGGCCCTTGCGCTA GAGCTGCAGTGGCTGGACATGAAG GTTTCTCTGT&lt;3' (SEQ ID NO:3)</pre>	<pre>5' &gt;CAGCACTGACTCTGACAGCTA TCGCAGTGGACCGCCACCAGGTGA GAGCACCTGCCCCAGCAGCATGC TCCCACATCTCCGTCTATGCCCTGGCT GGCTGGTGGGAATACTGCCACAC GGTCTGTAGGGAAATACTCTCAGGA CACTGACTCATTCAAGTCCCGCTGA CAGCGTGTGTGCTTGCCCTCCTTGT TGATCAATTG&lt;3' (SEQ ID NO:4)</pre>
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FIGURE 2B